

FIG.1



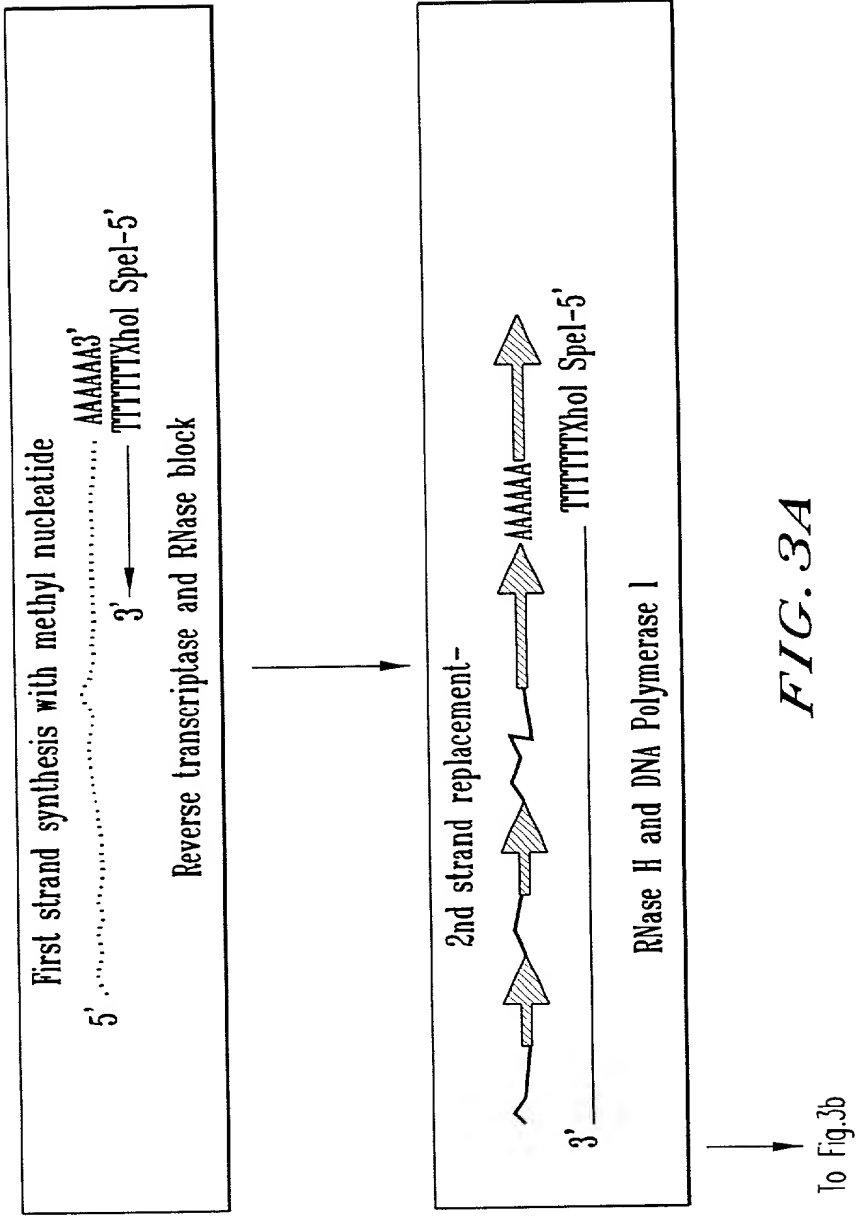


FIG. 3A

To Fig. 3b

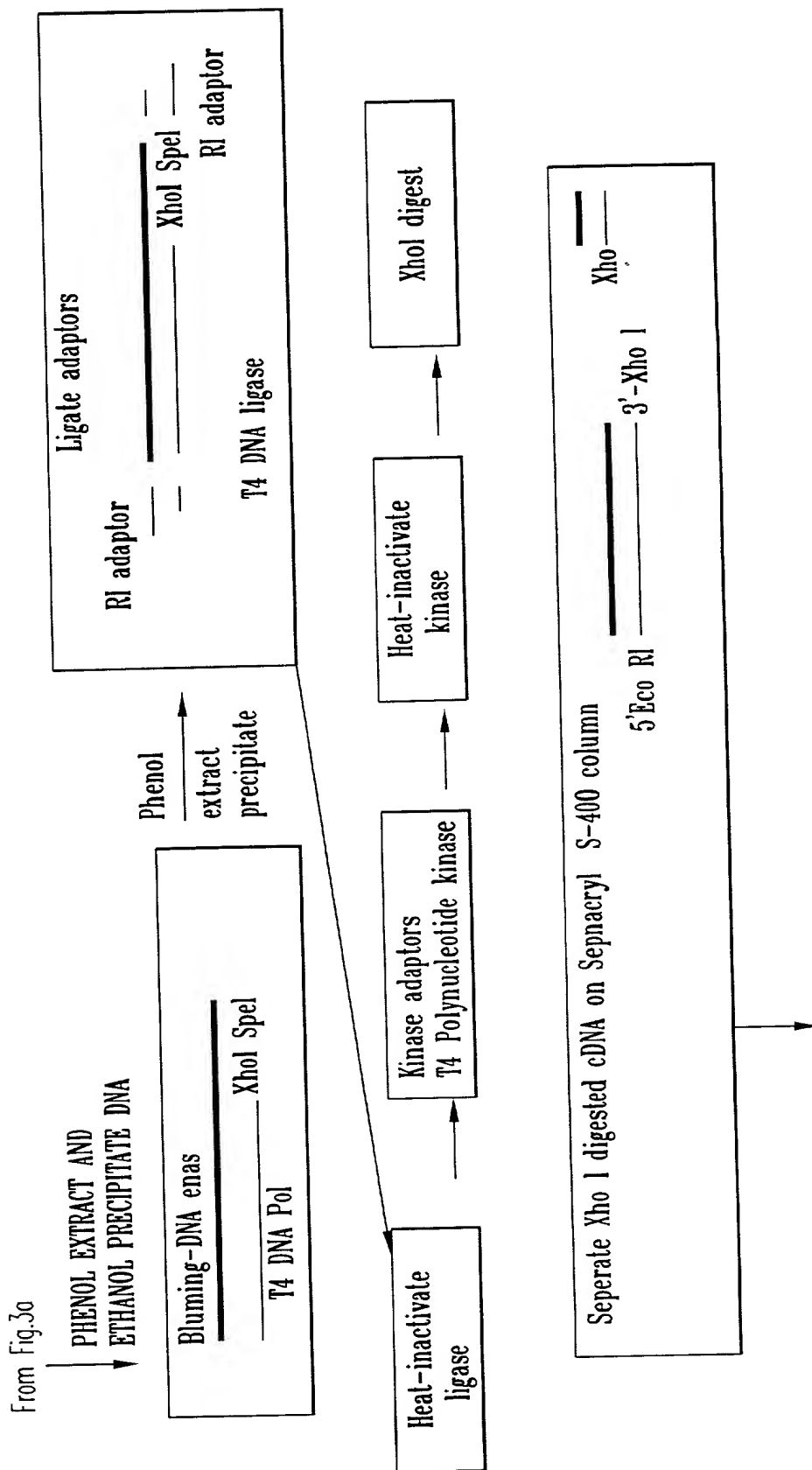


FIG. 3B

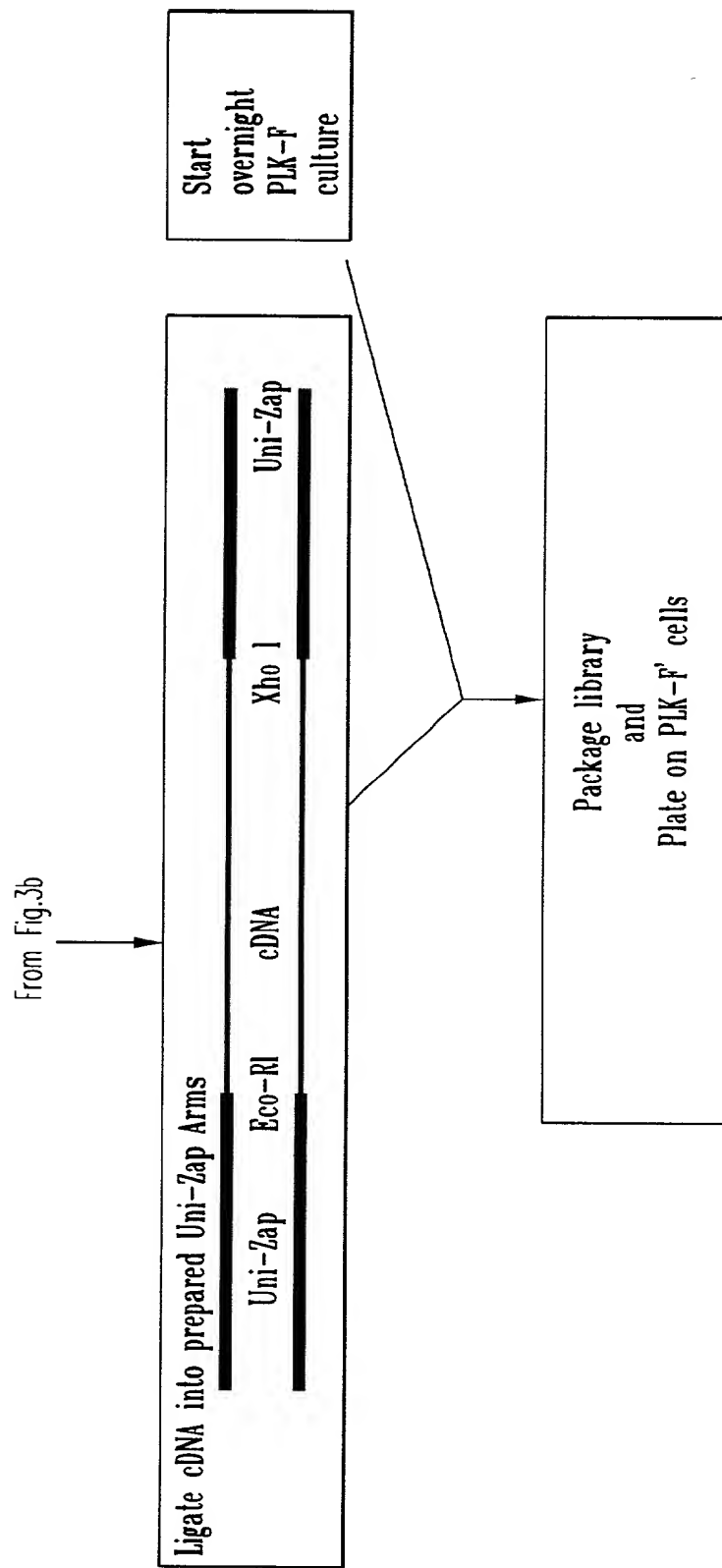


FIG. 3c

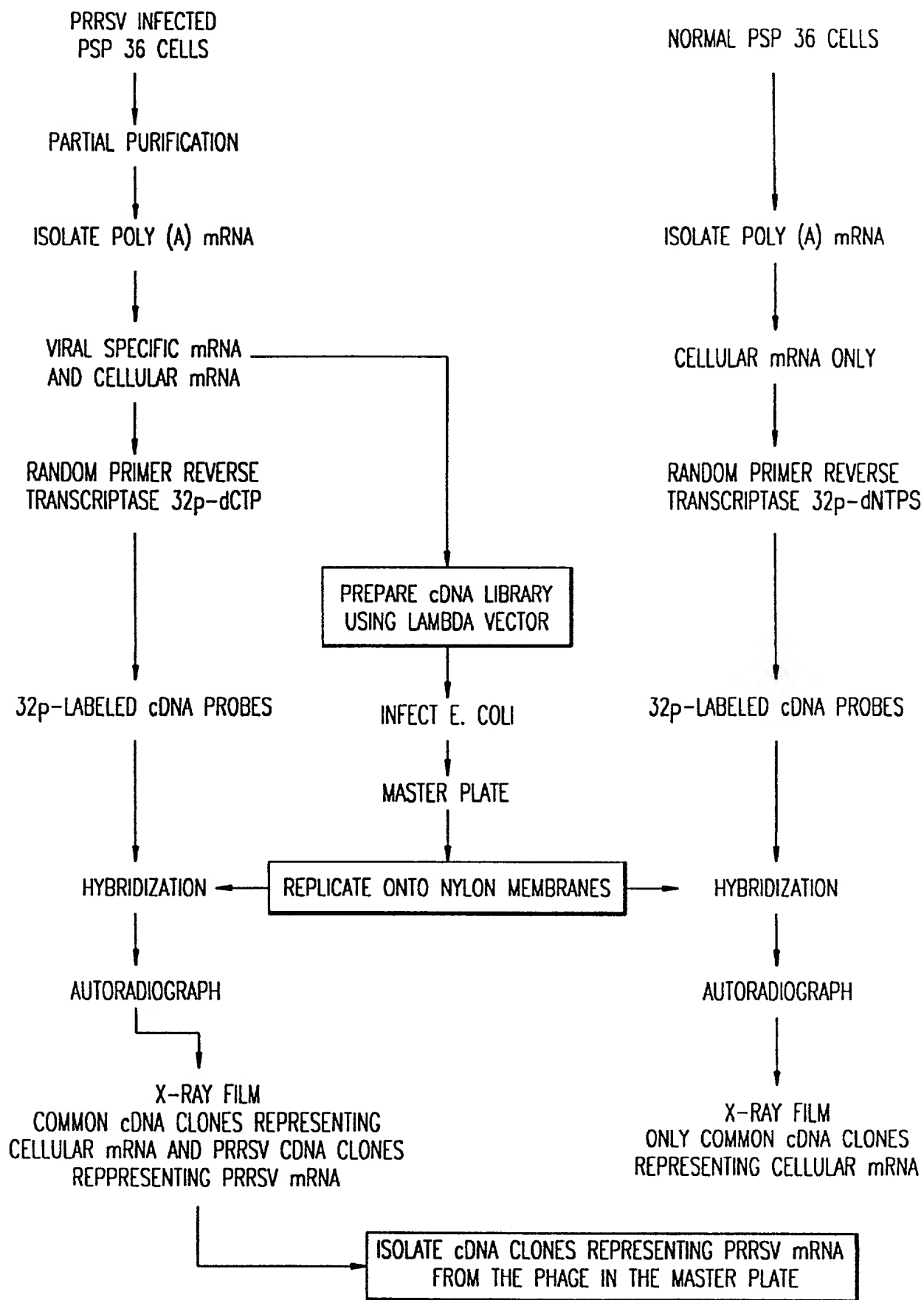


FIG.4

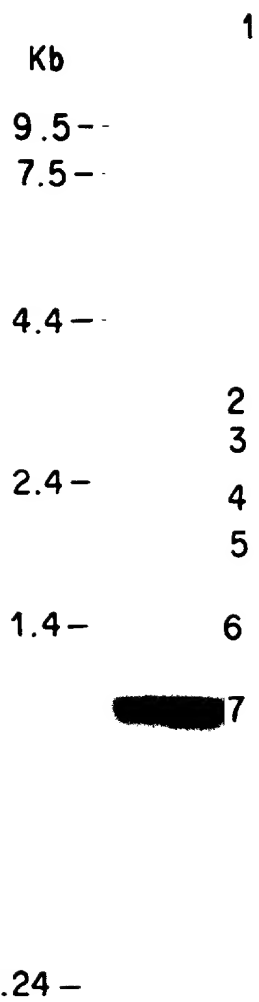


FIG.5

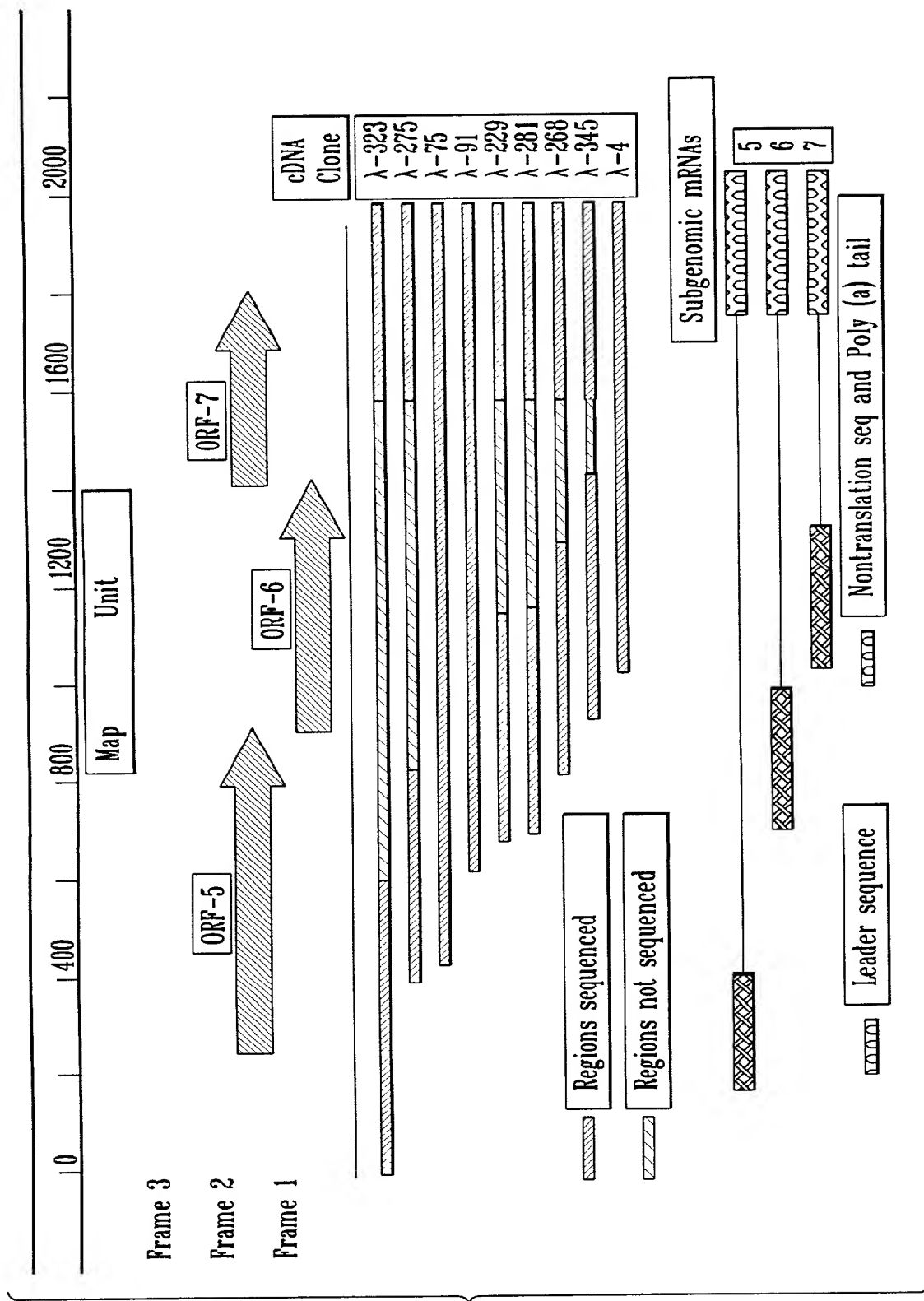


FIG. 6



GGCAGGCTTGGTGTCTCCAAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCGAGGCGATTGCGAAGTCCCCTCAGTGC CGCACGGCGGATAGGG 100

ACACCGGTGATATCACTGTCAACAGCCAAATGTTACCGATGAGAAATTATTGGATTCCCTCTGATCTTCTCATGCTTCTTCTTGCCCTTTTCTATGCTTCTG 200

AGATGAGTGAAGAAGGGATTAAAGGTGGTATTTGGCAATGTGTCAAGGATCGTGGCAGTGTGGCTCAACTTACCAGTTACGTCCAACATGTCAAGGAATT 300

TACCCAACGTTCCTTGGTAGTTGACCATGTGCGGTGCTCCATTTCATGACGCCGAGACCATGAGGTGGGCAACTGTTTTAGCCTGTCTTTTGGCATT 400

DRF4 stop  
\*\*\* +1>DRF5 start

CTGTTGGCAATTTGAAATGTTAAGTAAGTTGGGGAAATGCTTGACCGGGGCTGTGCTCGCAATTGCTTTTTTGGGTGATCGTGGCGTCTTGTGTTT 500

GTTGGCTCGTCAGCGCCACAGGGACAGCGGCTCAAATTTACAGCTGATTTACAACTTGACGCTATGTGAGCTGAATGGGACAGATTGGCTAGCTAATA 600

AATTTGACTGGCAGTGGAGTGTTTGTGATTTTCCCTGTGTGACTCACATTGTCTCTATGGTGGCCCTCAGTACAGCCATTCCCTTGACACAGTGGG 700

TCGTGCTCACTGTGCTACCGCTGGGTTTGTTCACGGGGGTAIGTTCTGAGTAGCATGTACGGCGTCTGTGCCCTGGCTGGCTTGATTGTGCTTGGTCAATT 800

AGGCTTGGGAAGAAATGCAATGTCTGGGCTACTCATGTACCAGATATACCAACTTCTTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGGCTG 900

TCATCATAGAGAAAAGGGCAAGTTGAGGTGGAAGGTCACTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCCGGGGTACCCCTGTAAACCAGAGT 1000

DRF6 start  
+1> \*\*\*DRF5 stop

TTCAGCGGAACAAATGGAGTCGTCTTAGATGACTTCTGTGATGATGACGGCTCCACAAAGGTGCTCTTGGCGTTTCTATTACCTACACGCCAGTGA 1100

FIG. 7A

TGATATATGCCCTAAAGGTAGTCGGCGCGCGACTGCTAGGGCTTCGACCTTTTGGCTTCCTGAAATGGTCTTCCATTGCTGACATGACATTCGT 1200  
 GCACCTTCAGAGTACAAATAAGGTGCGGCTCAGTATGGGAGCAGTAGTTGCACCTCTTGGGGGGTGTACTCAGCCATAGAAACCTGGAAATTCATCACC 1300  
 TCCAGATGCCGTTTGTGCTTGCTAGGCGCGCAAGTACATTCTGGCCCCCTGCCACCACGTTGAAAGTGC CGCAGGCTTTCATCCGATTGCGGCAATGATA 1400  
 ACCACGCATTTGTGCTCCGGCTCCCGGCTCCACTACGGTCAACGGCACATTGGTGGCCCGGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTAA 1500  
 ACCAGGGAGTGGTAAACCTTGTTAAATATGCCAAATAACACCGGCAAGCAGCAGAGAGAGAAAGAGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600  
 GCTGGGTAAAGTATCGCTACCCAAAACCAAGTCCAGAGGCAAGGGACCGGGAAGAAAAAATAAGAGAAAAACCCGGAGAGGCCCATTTCCCTCTAGCG 1700  
 ACTGAAGATGATGTCAGACATCATTACCCCTAGTGAGGTCATTTGTGCTGTGTCATCCAGACCGCCTTTAATCAAGGGCGCTGGGACTTGCACCC 1800  
 TGTGAGATTGAGGAGGATAAGTTACACTGTGGAGTTAGTTGCTACGCATCATACTGTGGCCCTGATCCGGGTCACAGCATCACCCCTCAGCATGATG 1900  
 GGCCTGGCATTCTTGAGGCATCCAGTGTGTAATTGGGAAGATGCGTGGTGAATGGCAGCTGATTGACATTGTGCCCTTAAGTCACCTATTCAATTAGGGC 2000  
 GACCGTGTGGGGTAAGATTTAATTGGCGAGAACACACAGCGCCGAAATTAACCAAAAAAAAAA 2062

DRF7 start  
 +1> \*\*\*DRF6 stop

\*\*\*DRF7 stop

**FIG. 7B**

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACAAATGGGGCGTTCTTGACTCCGCACCTCTTGCTCTGGTGGCTTTTTTTCGTGTGA--	13556
ISU-12-3' TERMINAL (426-1028)	-----ATGTTGGGGAAATCTTTGACCGCGGCTTTTGCTCGCAATTTGCTTTTTTGTGGGTATC	485
LELYSTAD SEQ (13484-14089)	----CCGCTTTGTCCTGGT-DCTTTTCCGATGCAACGGCGACAGCTCGACATACCAATA-D-ATATAAIAACTTG	13624
ISU-12-3' TERMINAL (426-1028)	GTGCCGTCTTGTTTGTGGCTCGTTCAGCGCAACGGGACAGCGGCTCAAAATTACAGCTGATTTACAACTTG	560
LELYSTAD SEQ (13484-14089)	ACGATATCGGAGCTGAATGGACCGACTGGTTGTTCAGCCATTTTGGTGGGCAGTCGAGACCTTTGTGCTTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTGAGCTGAATGGACAGATTGGCTAGCTTAATAATTTGACTGGGCAGTCGAGTGTCTTGCTATTTT	635
LELYSTAD SEQ (13484-14089)	CCGGTTGCCACTCATATCCCTCTCAGTCGGTTTCTCACACACAGCCATTTTGTGACCGGCTCGGCTCTGGGCT	13774
ISU-12-3' TERMINAL (426-1028)	CGTGTGTTGACTCAGATTGCTCTGTATGGTGGCTTCAGTACAGCCATTTCCCTTGACACAGTCGGCTCTGGTACT	710
LELYSTAD SEQ (13484-14089)	GATCCACTGCAAGATTGTTGGCGGGGGGTAGTACTCTGCAGGCTCTACCGGCTTTGTGCTTTCCGAGCGGTTC	13849
ISU-12-3' TERMINAL (426-1028)	GTGCTACCGCTGGGTTGTTTCACGGGGGTATGTTCTGAGTAGCATGTACCGGCTCTGTGCCCTGGCTGGCTTG	785
LELYSTAD SEQ (13484-14089)	GATGTGTTTGTCATCCGTGCTGCTAAAAATTGGCATGGCTGCGGCTATGCCGTACCGGTTTACCAACTTCATT	13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTGGTCAATAGGCTTGGCAAGAAATTGCATGTCTTCCGCTACTCATGTACCAAGATATACCAACTTTCTT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTTTCATCGATGGAGTCTCCAAATAGTTGGTAGAAAAATTTGGGCAAGCCGAGTCCGAT	13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGGAGACTCTATCGTTGGCTTGGCTCCCTGTCCATCATAGACAAACGGGCAAGTTGAGGTCCGAA	935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCAACCATCAACATGTGTTCTCGAAGGGGTAAAGCTCAACCCCTTCACAGGACTTCGGTGA	14073
ISU-12-3' TERMINAL (426-1028)	GGTCACCTTGAATCGAAGCTCAAAAGAGTTGTCTTGTATGGTTCCGGCGCT-ACCCCTGTAAACAGAGTTTCAGCGGA	1009
LELYSTAD SEQ (13484-14089)	GCAATGGGAGCCCTAG-----	14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTGGTCCCTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AATGGAGTGG TCGTTACATG ACTTGTGTCA TGAATAGACG GGTCCACAAA AGGTGCTCTT -ATGG-CAGG --CGTAGACG ATTCTTGCAG CGATCCATATC GCGGCACAAA AGCTGGTGGT	947 14132
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GGGTTTCT ATTAACATACA CCGCAGTATGAT GATATATGCC CTAAAGGIGA GTCCGGGGCG ACCGTTTACC ATCACAATACA CACGTATTAAT GATATACGCC CTAAAGGTGT CACGGGGCGG	1007 14192
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTGCTAGGG CTCTGCACC TTTTGGTCTT CTGAAATGT GCTTCACT TCGGGTACAT ACTCTGGGG CAGTTCACCA TCCATAATAT TCTGAACATGT TCGTTACAT TCGGATACAT	1067 14252
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GACATTCGTG CACTTTCAGA GTAAATATAA GTTCGGCTC ACTATGGAG CAGTAGTTCG GACATATGTG CATTTTCAAT CCACCAACCG TGTCCGACAT ACCCTGGGGG CTGTTGTCG-	1127 14311
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTCTTTTGG GGGGTGTACT CAGC -CATTA GAACCTTGA ATTTATACAC CTCCAGATGC -CCCTTCTGT GGGGTGTCTTA CAGCTTCACA GAGTATGGA AGTTTATCAC TTCCAGATGC	1185 14370
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	CGTTTGTGCT TGTAGCCCG CAAGTACATT CTGGCCCCCTG CCCACACGT TGAAGTGC AGATTGTGTT GCCTTGGCCG GCGATACATT CTGGCCCCCTG CCCATCACGT AGAAAGTGT	1245 14430
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GCAGGCTTTTC ATCGGATTCG GGCATAATGAT AACCAAGCAT TTGTGTCTCG GCGTCCGGC GCAGGCTCTCC ATTATATCTC AGCGTCTGCT AACCGAGCAT AGCGTCTAG AAAGCCCGGA	1305 14490
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	TCCACTAGG TCAACGGCAC ATTGGTCCC GGGTTAAAAA GCCTCGTGT GCGTGGCACA CTACATCAG TCAACGGCAC TGTAGTACCA GGAATTCGGA GCCTCGTGT GCGCGGCANA	1365 14550
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AAMGCTGTTA AAGACGGAGT GGTAAACCTT GTTAATATG CCAAAATA CCAGCTGTTA AAGACGGAGT GGTAAACCTC GTTAAGTATG GCGGTAA	1413 14598

FIG.9

Lelystad seq (14588 – 14974)	ATGGCCGGTA AAAACCAGAT- GCCACAAAGAA AAAGAAAGT A-CAG-----C 14632
ISU 12/7a/3' terminal (1403 – 1774)	-----AT GCCAAATTAAC ACCGGCAAGC AGCAGAAGAG 1434
Lelystad seq (14588 – 14974)	TCCGATGGGG AATGGCCAGC CAGTCAATCA ACTGTGCCAG TTGCTGGGTG 14681
ISU 12/7a/3' terminal (1403 – 1774)	AAAGAGCGGG CATGGCCAGC CAGTCAATCA GCTGTGCCAG ATGCTGGGT- 1483
Lelystad seq (14588 – 14974)	CAATCATAA GTCCACGCC CACCAACCTA GCGG--A-GG AAGGCCCAAA 14728
ISU 12/7a/3' terminal (1403 – 1774)	-AA-GATCAT CGCTCAGAA AACAGTCCA GAGGCAAGG ACCGG---GA 1528
Lelystad seq (14588 – 14974)	AAGAAAAA-- ----G----- -CCTGAGAAG CACATTITTC CCGTGGGTGG 14766
ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAAATA AGAAGAAAAA CCGCGAGAAG CCGCATTTCC CTCIAGCGAG 1578
Lelystad seq (14588 – 14974)	TGAAGATGAC ATCCGGCACC ACCTACCCCA GACTGAAGCG TCCGTCTGCT 14816
ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAT GTACAGATTC ACTTTACCCC TAGTGACCGT CAAATTGTGTC 1628
Lelystad seq (14588 – 14974)	TCCAATTCAT CCAGACCGGT TTCAATCAAG GCGCAGGAAG -TGGCTGGCT 14865
ISU 12/7a/3' terminal (1403 – 1774)	TGTGCTCAT CCAGACCGCC TTTAATCAAG GCGCTGGGAG TTGCAAG-CT 1677
Lelystad seq (14588 – 14974)	TTTCATCCAGC GGAAGGTCA GTTTTCAGGT TGAGTTTATG CTGCCGTTG 14915
ISU 12/7a/3' terminal (1403 – 1774)	GTCAGATTCA GGGAGGTTAA GTTACACTGT GGAGTTTATG TTGCCGTACGC 1727
Lelystad seq (14588 – 14974)	CTCATAAGT GCGCCCTGATT CCGGTGACTT CTACATCCGC CAGTCAGGT 14965
ISU 12/7a/3' terminal (1403 – 1774)	ATCATACTGT GCGCCCTGATC CCGGTGACAG CATCACCG-T CAG-CATGA- 1774
Lelystad seq (14588 – 14974)	GCAAGTTAA 14974
ISU 12/7a/3' terminal (1403 – 1774)	1774

FIG.10

ISU 12/7a/3' terminal (1775 – 1938)	TGGGCTGGCA TTCTTGAGGC ATCCAGTGT TTGAATTGGA	1814
Lelystad seq (14975 – 15101)	-----	14976
ISU 12/7a/3' terminal (1775 – 1938)	ACAAATGGCTG GTCAATGGCA CTGATTGACA TTGTGCCTCT	1854
Lelystad seq (14975 – 15101)	TGACAGTCAG GTCAATGGCC GCGATTGGCG TTGTGCCTCT	15016
ISU 12/7a/3' terminal (1775 – 1938)	AAGTCACCTA TTCAATTAGG GCGACCGTGT GGGGGTACGA	1800
Lelystad seq (14975 – 15101)	GAGTCACCTA TTCAATTAGG GCGATCACAT GGGGGTCAATA	15056
ISU 12/7a/3' terminal (1775 – 1938)	TTTAAATT-GG GGAGAACCAC ACACCGGAAA TTAAAAAAA	1933
Lelystad seq (14975 – 15101)	CTTAAATCAGG GAGCAACCAT GTACCGGAAA TTAAAAAAA	15096
ISU 12/7a/3' terminal (1775 – 1938)	AAAAA	1938
Lelystad seq (14975 – 15101)	AAAAA	15101

FIG. 11

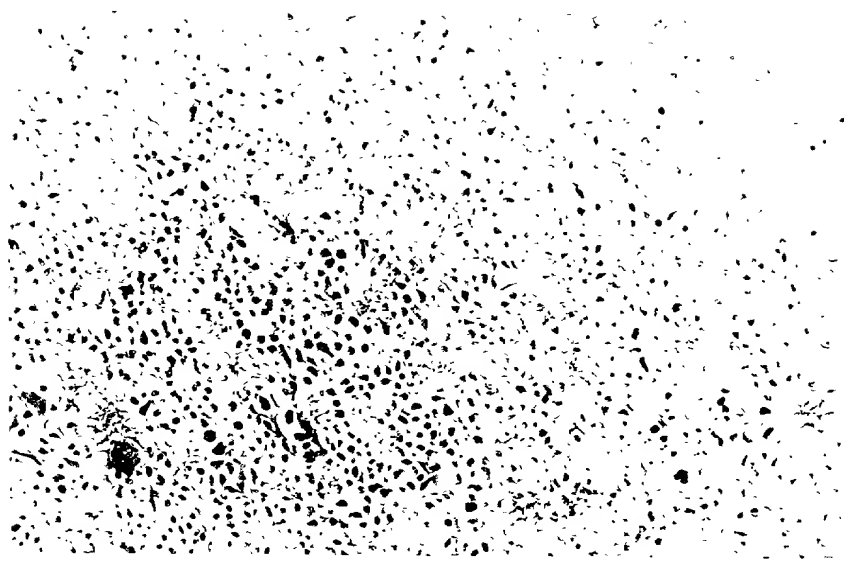


FIG.12

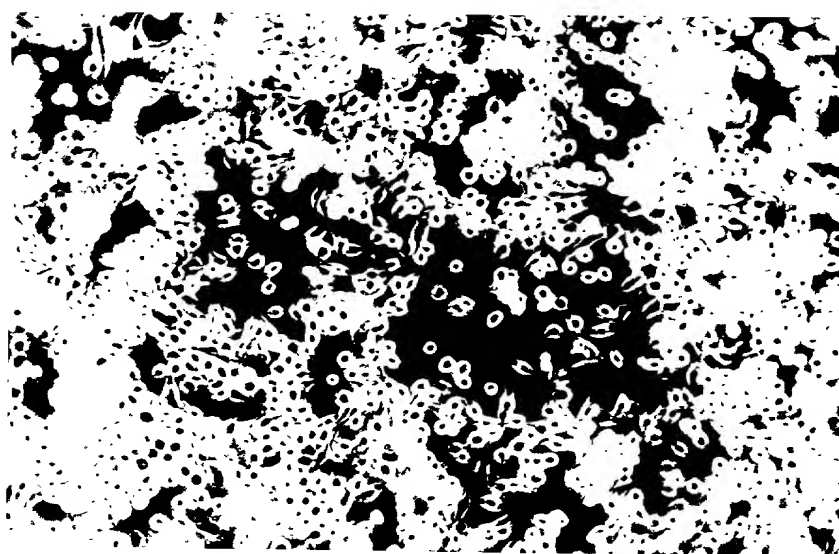


FIG.13



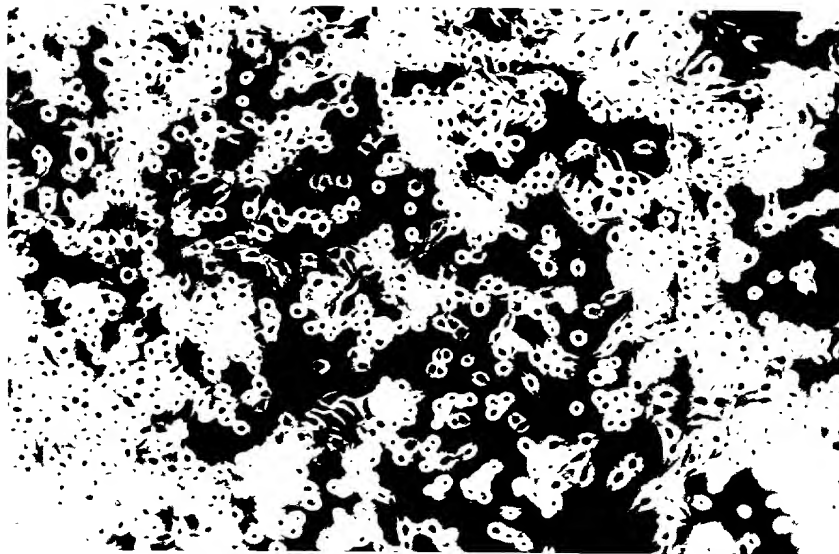


FIG.14

SM E M NP E+M+NP SM

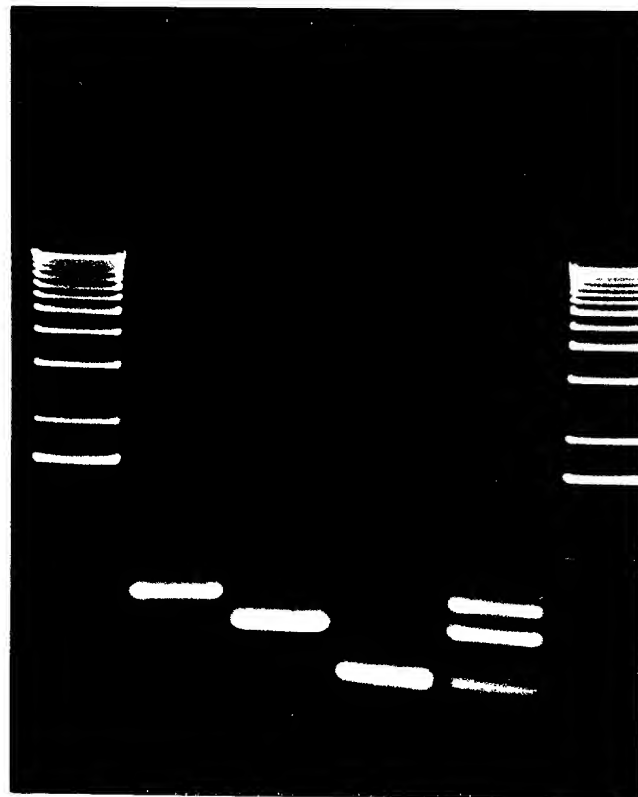


FIG.15

SM pVL1393 E M NP SM

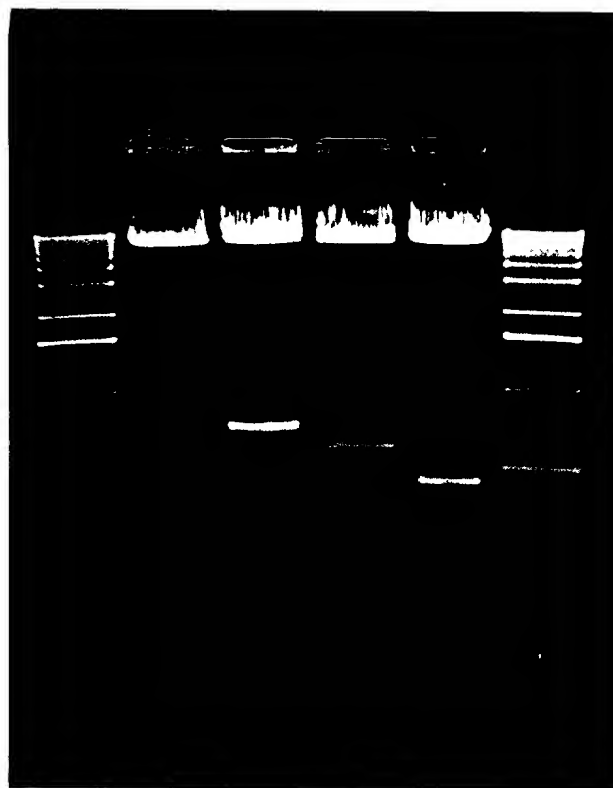


FIG.16

VR 2385	GTTTGTGCTTGCTAGGCGCAAGTACATTCTGGCCCTGCCACCACGTTGAAAGTGCCGAGGCTTTCATCCGATTGCGGCAAAATGATAACCACGCGATT	398
ISU-1894	.....	398
ISU-22	.....	398
ISU-79	.....	398
ISU-55	.....T.....A.....	398
ISU-3927	.....G.....	398
LV	A.....T.GC..T.....GCGA.....T.....A.....T.C.C..T.A..CT.A..GTC..G.....GA....A	395
VR 2385	TGTGTCGCGGCTCCCGGCTCCACTAGGCTCAACGGCACATTGGTGCCCGGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTTAAACAGGGAGTG	498
ISU-1894	.....G.....	498
ISU-22	.....T.....G.....	498
ISU-79	.....G.....	498
ISU-55	.....T.....G.....C.....	498
ISU-3927	.....T.....G.G.....A.....G.....	498
LV	C.CT..GA.AAAG.....ACTA..AT.A..G.....TC.A..A..A..AC..TCGG.....C.....C.....A.CG.....GA.....	495
DRF 7 start		
VR 2385	GTAACCTTGTTAAATATGCCAAAATACACCGGCA-AGCAGCAGAGAGAGAAAGAA-----GGGGGATGGCCAGCCAGTCAATCAGCTGTG	582
ISU-1894	.....C.....A.....A.....	582
ISU-22	.....C.....A.....A..T..-	582
ISU-79	.....C.....A.....A.....-	582
ISU-55	.....C.....A.....A.....A.....-	582
ISU-3927	.....C.....A.....A.....A.....-	582
LV	.....T.....C..C..G.....G.CGG..A.A..--..G.....A.....AAGTACAGCTCCCGAT.....A.....A.....	591

FIG. 17B

VR 2385	CCAGATGCTGGGT--AA-GATCATCGCTCACCAAACCAAGTCCAGAGGCAAGGACCGGGAAAGAAAAATAAGAAGAAAACCCGGAGAGCCCATTTTC	679
ISU-1894	.....G.....C.....	T 679
ISU-22	.....C--.....T.....	T 679
ISU-79	.....C.....T.....	T 679
ISU-55	.....C.....C.....	T 679
ISU-3927	A.....C.....T.....	T 679
LV	....T.....GC..T...A.AGT.C.G.---G.....-..-..CCT.G.....C....GCC..A.....G..T.....A.....T	679

VR 2385	CCTCTAGCGACTGAAGATGATGTCAGACATCACTTTACCCCTAGTGAGGTCATTTGTCGTCAATCCAGACCGGCTTTAATCAAGGGCTGGGA	779
ISU-1894	.....C.....G.....	779
ISU-22	.....G.....	779
ISU-79	.....G.....A..T.....	779
ISU-55	.....C..T..G.....G.....A.....A.....	779
ISU-3927	.....C.....C.....G.....T.....G.....	779
LV	..C..G..TG.....CA..C.G..C.C...AG.C...A..CTCCC.C..CT..CAA..G.....G..T..C.....A..A..	779

FIG. 17C

VR 2385	CTTGCACC-CTGTCAGATT	CAGGGAGGATAAGTTACACTGTGGAGTTAGTTTGCTAGGCATCATACTGTGGCGCTGATCCGCGTCACAGCATCACCC-	877
ISU-1894	.....	.....A.....T.....	877
ISU-22	.....	.....	877
ISU-79	.....	.....T.....	877
ISU-55	.....T.....	.....G.....G.....	877
ISU-3927	.....C...T...T...A.....	.....G.....T.....G...C.....	877
LV	.....-...GT...G...T...TCCAGC...A...G...C...TTCAG...T...TGC...GGTTGC...A.....	.....G...TT...TA...T...G	878

VR 23 85	TCAG-CA-----TGA	*** ORF 7 stop	886
ISU-1894	.....-...-----		886
ISU-22	.....-...-----		886
ISU-79	.....-...-----		886
ISU-55	.....-...-----		886
ISU-3927	.....-...-----		886
LV	C...T...GGGTGCAAGT...A.....		898

FIG. 17D

VR 2385 DRF6 MESSLDDFCHDSTAPQKVLLAFSITYTPVMIYALKVSRGRLLGLLHLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAWALLWGVYSAIETWKFITSRCR 100  
 ISU-1894 DRF6 , G.....I..... 100  
 ISU-22 DRF6 , G.....I..... 100  
 SIU-55 DRF6 , G.....I..... 100  
 ISU-79 DRF6 , G.....Y.....M..... 100  
 ISU-3927 DRF6 , G.....N.....I.....E...R..... 100  
 LV DRF6 , G-G.....N.PI.A.,LV.....I.....S.....Y.....R...L.....FT,S..... 99  
 PRRSV-10 DRF6 , G-G.....N.PI.A.,LV.....I.....S.....Y.....R...L.....FT,S..... 99  
 LDV-C DRF2 , G-G,-E.,DQTSWY,-IFI.,L....IA.,S.,F.,T.A.IVNIFI.,I.,CVS.V,LMYH,-SV.,TI.,SL.,I.,V.,I.,TLVKIVDWLVI,... 96  
 LDV-P DRF2 , G-G,-E.,DQTSWY,-I.I.,L....IA.,S.,F.,T.A.IVNIFI.,I.,CVS.V,LMYH,-SV.,TI.,SL.,I.,V.,I.,TLVKIVNMWVL,... 96

VR 2385 DRF6 LCLLGRKYILAPAHHVESAAGFHP IAANDNH-----AFVRRPGSTTVNGTLVPGLSLVLGGRKAVKQGVVNL VKY-AK 183  
 ISU-1894 DRF6 ,.....-----,.....-., 174  
 ISU-22 DRF6 ,.....-----,.....-., 174  
 SIU-55 DRF6 ,.....-----,.....-., 174  
 ISU-79 DRF6 ,.....-----,.....-., 174  
 ISU-3927 DRF6 ,.....-----,.....R.....K.....-., 174  
 LV DRF6 ,C.,R.....L.S.,SG,R-----,YA.,K.,L.S.....R.....KR.,R.....-GR 173  
 PRRSV-10 DRF6 ,C.,R.....L.S.,SG,R-----,YA.,K.,L.S.....R.....KR.,R.....-GR 173  
 LDV-C DRF2 ,F.,S.,PS.,D-----TSDGRQSLTTSITI.,K.,L.,Q.,DFQR.,K.,SK,A.,L.,VS., 171  
 LDV-P DRF2 ,F.,S.,PS.,D-----TSDGRQSLTTSITI.,K.,L.,Q.,DFQR.,K.,SK,A.,L.,VS., 171

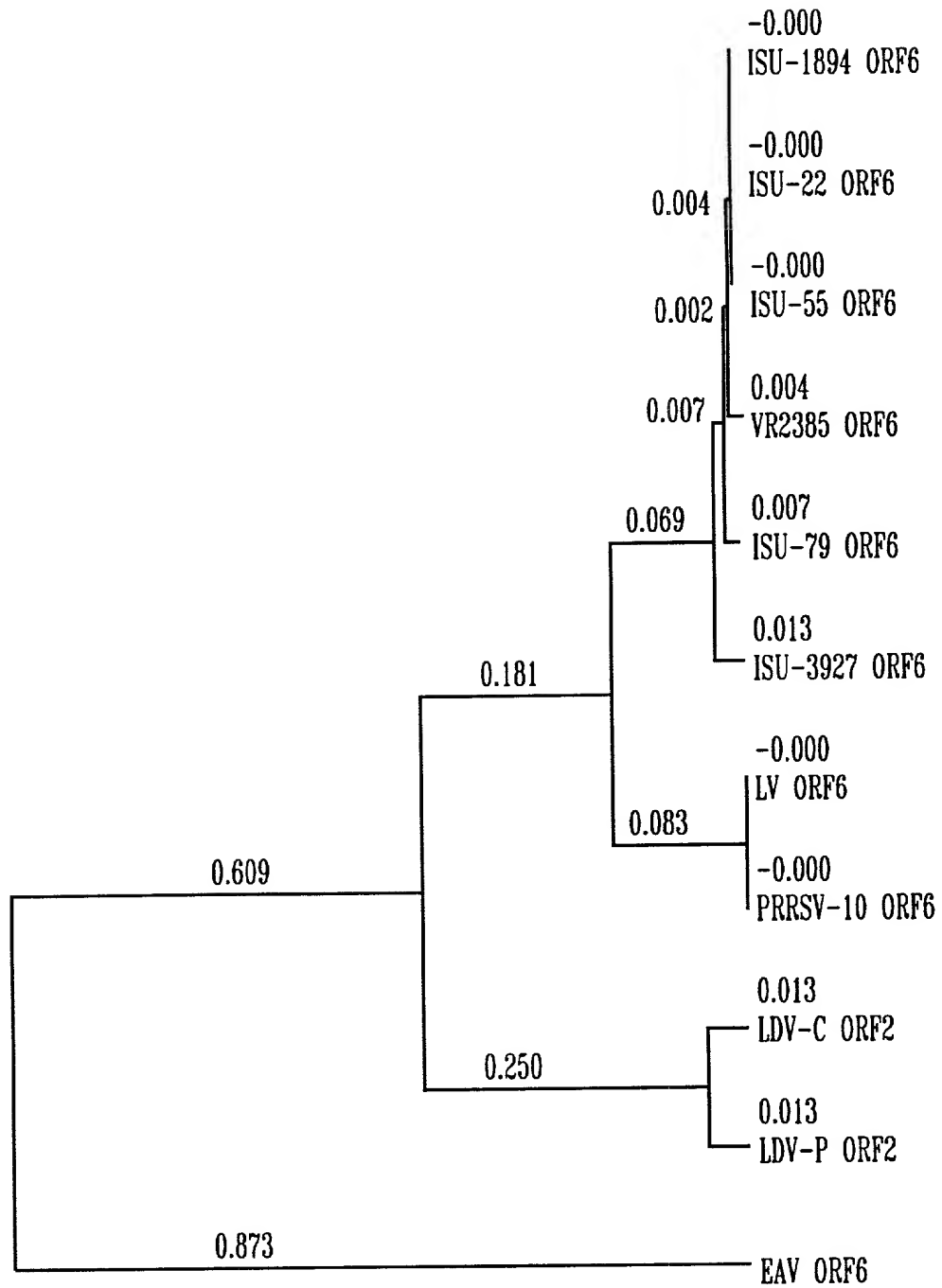
FIG. 18A

VR 2385 DRF7 MPNNTGQQRKK-----GDGPVNQLCQMLGKIIAHQNSRGKGPCKKKNKKNPEKHPFLATEDDVRHHFTPSERQLCLSSIQTAFNQGAGTCTLS 100  
 ISU-1894 DRF7 .....N.....Q..... 93  
 ISU-22 DRF7 .....N.....Q..... 93  
 ISU-79 DRF7 .....N.....Q..... 93  
 ISU-3927 DRF7 .....N.....K.....Q.....I.. 93  
 ISU-55 DRF7 .....N.....K.....Q.....SG..... 93  
 VR2332 DRF7 .....N.....TEE.....Q..... 93  
 LV DRF7 ---A..N..SQ..KKSTAPM..N.....L..AM.KS.R.---QPR.GQA..K.....A..I...L..QT...S...Q.....AS... 94  
 PRRSV-10 DRF7 ---A..N..SQ..KKSTAPM..N.....L..AM.KS.R.---QPR.GQA..K.....A..I...L..QT...S...Q.....PS... 94  
 LDV-C DRF1 ..SQ.KK.GGQN,-----AN,---..N.LISALLRNAG,---N..K.Q.K.,-Q,-L...M.GPS.L..VM..N.V.M.R..LV.L...G.Q...V 85  
 LDV-P DRF1 ..SQ.KK.SGQN,-----AN,---..N.LINALLRNAG,---N..K.Q.K.,-Q,-L...M.GPS.L..VM..N.V.M.R..LV.L...G.Q...V 85  
 EAV DRF7 .ASRRSRP.AASF-----RN.R--RRQPTSYNDLLRMFG,-----MRVR.PPAQPTQAI.I.EPG.L.,DLNQQ.,ATLS.NV.RF.MI.H.SL.-A 83  
 ^^^^^^

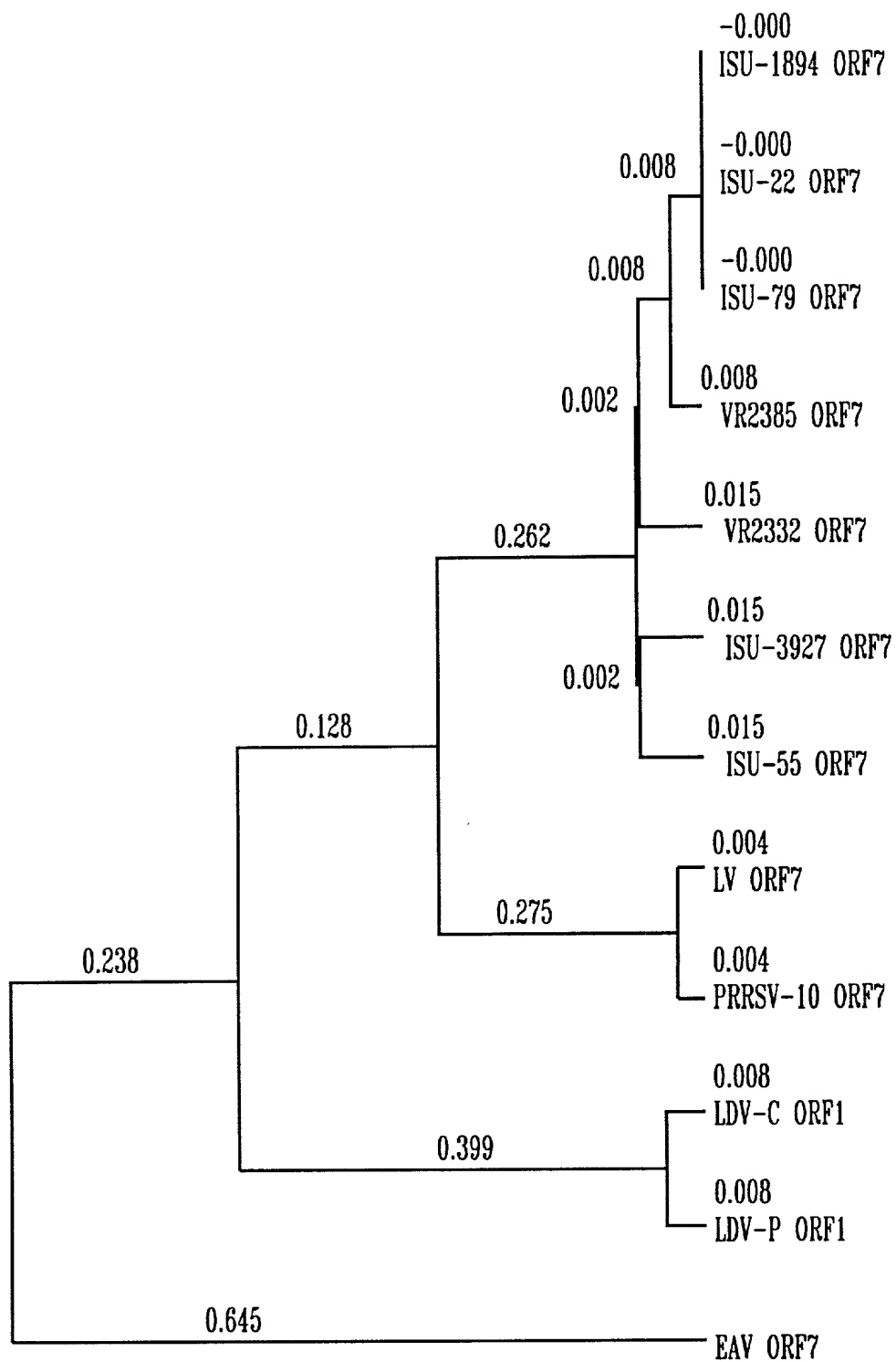
VR 2385 DRF7 DSGRISYTFESLPTHTVRLIRVTASP----SA 134  
 ISU-1894 DRF7 ..... 123  
 ISU-22 DRF7 ..... 123  
 ISU-79 DRF7 ..... 123  
 ISU-3927 DRF7 .....P..... 123  
 ISU-55 DRF7 ..... 123  
 VR2332 DRF7 ..... 123  
 LV DRF7 S..KV.FQ...M..VA.....STSASQGS 128  
 PRRSV-10 DRF7 S..KV.FQ...M..VA.....STSASQGS 128  
 LDV-C DRF1 ...G.NF..S.M...A.....NAS.NS----, 115  
 LDV-P DRF1 ...G.NF..S.M...A.....NAS.NS----, 115  
 EAV DRF7 .A.GLT...SW-V..KQIQ.KVAPP.G,----- 110  
 ^^^^

FIG. 18B





*FIG. 19A*



**FIG. 19B**

+ Start ORF2  
 CCTGAATTGAGATGAGGATGCGGCTATGCAAGCCTTTTGACAAAAATGGCCAACTTTTTGTGGATGCTTTCACGGAGTTCTTGGTGTCCATTGTTGAT 100  
 ATCATTATATTTTTGGCCATTTGTTGGCTTCACCATCGCAGGTTGGCTGGTGGCTTTTGGCATCAGATTGGTTGGCTCCGGGATACTCCGTTGGCGGCC 200  
 CTGCCATTCACTCAGCAATTACAGAAAGATCCTATGAGGCCTTTCTCTCAGTGCCAGGTGGACATTCACCCTGGGGAACTAAACATCCTTTGGGGA 300  
 TGCCTTGGCACCATAAGGTGTCAACCTGATTGATGAATGGTGTGCGTGAATGTACCGCATCATGGAAAAAGCAGGACAGGCTGCCGTGGAAACAGGT 400  
 AGTGAGCGAGGCTACGCTGCTCGCATTAGTAGTTGGATGGTGGCTCATTTTCAGCATCTTGGCGCCATTGAAGCCGAGACCTGTAAATATCTGGCC 500  
 TCTCGGCTGCCCATGCTACACCACCTGCGCATGACAGGCTCAAAATGTAAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTTGGCTGTTTCCCAACCC 600  
 CTGGTCCCGGCCAAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCCTCTATATTTTCCCTGTTGCAGCTTCTTGTACTCTTTTGTGT 700  
 + Start ORF3  
 GCTGTGGTTGCGGGTTCCAATGCTACGTACTGTTTTTGGTTTCCGCTGGTAGGGGCAATTTTCTTTCGAACTCAGGTTGAATTACACGGTGTGGCCG 800  
 CTTGCCCTACCCGGCAAGCAGCCGCAGAGGCCCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATCGATGTGGGAGGACGATCATGATGA 900  
 ACTAGGGTTTGTGTGGCTCTCGGCTCTCAGCGAAGGCCACTTGACCAGTGCTTACGCCCTGGTTGGCGTCCCTGCTCCTTCAGCTATACGGGCCAGTTT 1000  
 CATCCCGAGATATTCGGGATAGGGAATGTGAGTCGAGTCTATGTTGACATCAGCACCAATTCATTTGGCGTGTTCATGATGGGAGAACACCACCTTGC 1100

\*\*\* Stop ORF2

FIG. 20A

+ Start DRF4  
 CCCACCATGACAACATTTACGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTACCTAGAATGGTGGTGCCCTTCTTTC 1200  
 CTCCTGGTTGGTTTTAAATGTCCTCTGGTTCTCAGGGCTTCGGCTGCAAGCCATGTTTCAGTTCGAGTCCTTCAGACATCAAGACCACACACCACCGCAG 1300  
 \*\*\* Stop DRF3  
 CGGCAGGCTTTGCTGTCTCCAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCTGAGGCGATTGCAAAAGTCCCTCAGTGGCGCAGCGGATAGG 1400  
 GACACCCGTGTATACACGTGCACAGCCCAATGTTACCGATGAGAATTATTGGCATTCCTCTGATCTTCATGCTTTCCTTGGCTTTTCATGCTTCT 1500  
 GAGATGAGTGAAAAGGGATTTAAGGTGGTATTTGGCAATGTTGTCAAGGCATCGTGGCAGTGTGGGTCAACTTACCAGTTACGTCCAACATGTCAAGGAAT 1600  
 TTACCCAACGTTCCCTTGGTAGTTGACCATGTGGGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTTAGCCGTCTTTTTTACCAT 1700  
 \*\*\* Stop DRF4 + Start DRF5  
 TCCTGTGGCAATTTGAATGTTAAGTATGTTGGGGAAATGCTTGACCGCGGGCTGTTGCTCGCAATTGCTTTTTTATGGTGTATCGTGCCGCTTGTT 1799

*FIG. 20B*

Consensus	ATGMAATGGGGTCWMTGYRRAGCCTTTTGAYAAAATYRGCCARCTKTTYGTGGAYGCTTCACKGAGTTCYTKGKWSYRTKGTGATATYRYATWTT	100
VR2385 DRF2	...A...TA...CAA...C...TG...A...T...T...G...GTCCA...T...CATT...A...	100
LV DRF2	...C...AC...TGG...-----T...CA...G...C...C...T...TAGTG...G...TGC...T...	91
Consensus	YYTKGCCATWYTGTTGGSTTACCRTCCAGGWTGGYTRSTGGTCTTYKYMTCAGAKTGTTGTCCGGGMTWCTCCGTCGGCCYCTGCCATTAC	200
VR2385 DRF2	TT...G...TT...C...A...T...C...GG...TGCA...T...A...G...C...	200
LV DRF2	CC...T...AC...G...G...A...T...AC...CTTC...G...C...T...T...	191
Consensus	TCTSMSSAAYTAYMGAAGRTCCATGARGSCCTKYTSYCYMASTGCMRRSYGGAYAKTCCACAMTKKGSARYAARCAAYCCWTTGGGKATGYTTGGCA	300
VR2385 DRF2	...GAGC...T...CA...A...G...C...TC...CT...TC...G...CAGGT...C...T...-C...GG...G...ACT...A...T...T...G...C...	299
LV DRF2	...CCCG...C...TC...G...A...G...GT...GC...CA...C...AGACC...T-G...A...TT...C...GTC...G...C...A...T...T...	290
Consensus	CCATRMGAGTKTCMMMYCTGATTGATGARATGGTSTCKCGTCGMATKTACCRSAYCATGGAAMWKCAGGWCARGCKGCTGGAAARCAGGTGTRGTRGYGA	400
VR2385 DRF2	...AA...-...G...AAC...C...A...G...G...A...G...GC...T...A...AG...A...G...T...A...A...A...GA...C...	398
LV DRF2	...-...GC...T...CCA...T...G...C...T...C...T...AG...C...T...T...T...A...G...G...G...G...T...G...T...	389
Consensus	GGCYACGCTSTCWCMAKYWGTGAGGKYTSGATRTGTRGTRGTRCTATTTTCARCACTKGGCCGCMRTKGARCGSGAKWCYTGYNMTWTCTSRSCCTCWGRC	500
VR2385 DRF2	...T...G...T...C...TTA...-...-...TT...G...G...G...G...T...G...T...T...CA...T...A...C...GA...C...TAAA...A...GGC...T...G...	496
LV DRF2	...C...-...C...A...A...GCT...GC...C...A...A...TA...C...A...C...G...AG...G...G...T...T...T...CCGC...T...CAG...A...A...	487

FIG. 21A

Consensus	TSSYSATGCTAMAMMAYCTGYGCATGWYAGGGTCAAAATGTRASCMTASWGTAYAAAYASYACKTTGRAYCRSGTGTKWGCTCRTYTTCCCMACSCCWGGTW	600
VR2385 DRF2	, GCCC, . . . . . C, CC, C, . . . T, AC, . . . . . A, C, A, GT, . . . T, I, GT, . . . A, T, AG, . . . TT, . . . -G, I, . . . A, C, , T, . . . T	595
LV DRF2	, CGTG, . . . . . A, AA, T, . . -T, . . -C, TT--., -, -, . . . . . G, G, C, CA, . . C, C, CC, G, . . G, C, GC, . . -GA, . . . . . A, C, . . . . . C, G, A, . . . A	580
Consensus	CSMGGCCMAAGYTKMMYGATTTCMRRCATGGCTMATMRSTGIRCAKCYTCYATWTTTCCICIGTKGCKWCCTCKKTACYTKTYRTWTGTGCTKTG	700
VR2385 DRF2	, CC, . . . A, . . C, TCAT, . . . . . CAG, . . . . . A, AGC, . . . A, TT, C, T, A, . . . . . T, AG, T, . . TG, . . TC, I, . . TG, I, . . . . . G, .	695
LV DRF2	, GA, . . . C, . . T, GACC, . . . . . AGA, . . . . . C, CAG, . . G, CG, T, C, T, . . . . . G, TT, A, . . GT, . . . CT, G, CA, A, . . . . . T, .	680
Consensus	GYTKCGRRITCCARYKCTACGYWMGTGTTTTGGTTTCCRYTGGYYMRSGGCAAYWWTCWTTTCGARCTSACGGTGA	776
VR2385 DRF2	, T, G, GG, . . . . ATG, . . . . TAC, . . . . . . . . . . GC, . . . TAGG, . . . . . TTTT, . . T, . . . . . A, C, . . . . .	771
LV DRF2	, C, T, AA, . . . . . GCT, . . . . . CTA, . . . . . . . . . . AT, . . . CCCAC, . . . . . CACA, A, . . . . . G, G, -----	750

**FIG. 21A. 1**

Consensus	ATGGCTMATMRSTGTRCAYKCYTCYATWTTTTCCCTCTGTGCKWKCWCTCKTACYYTKTYRTWTGCTGTGGYTKCGRRTTCCARYKCTACGYWMTGTT	100
LV DRF3	.....C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT..G..CA.A....T...C.T..AA....GCT.....CTA....	100
VR2385 DRF3	.....A..AGC...A..TT.C..T..A.....T..AG.T...TG...TC.T...TG.T.....G...T..G..GG....ATG.....TAC....	100
Consensus	TTTGGTTTCCRYTGGYYMRSGGCAAYWWTCTTCGARCTSACSRTSAAYTACACSRTRTGCHGCCYTGYYYACCMGKCAAGRGCTCGCMRARGSCT	200
LV DRF3	.....AT...CCCAC.....CACAA..A....G..G..CA.C..C....CA.A..AT...C..TTCT...A.T....G.....CA.A.G..	200
VR2385 DRF3	.....GC...TTAGG.....TTTT..T.....A..C..GG.G..T.....GG.G..CC...T..CCTC...C.G....A..-...AG.G.C..	199
Consensus	ACGARCCCGGYMGKWMCMTKTGTGTCARRATAGGGCATGAYMGRGTGTGRGGAGSRYGAYCATGATGARYTAGKKWWTGTCSTSCCGTCYGGSYWCKMCA	300
LV DRF3	-...G....TC.TAA.A.G.....AA.....CA.G....A....CGT..C.....GT..-..TTAA....CA.C....C..GTA.GA..	298
VR2385 DRF3	....A....CA.GTC.C.T.....GG.....TC.A....G....GAC..T.....AC...GGTT...-GG.G....T..CCT.TC..	298
Consensus	sRCGAMKSMMACTTGACSRGTKMTTAYGCTGGYTGCGKTYYYTGCTTYWCTAYRCGGCCARTTCCATCCSGAGWTRTTCGGGATAGGGAATGTGWS	400
LV DRF3	A.--CTCAA.....-GG..TA...T..T...C...T.TTT.....TTC...CG.....A.....G...T.G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C...T....G.CCC.....CAG..TA.....G.....C...A.A.....AG	398
Consensus	KCGMGTCTWYGTGACAWSMRRCAACCACTTCATTGTGYGYGKWCATGATGRCASAAAYWCMACCKTRYCYMCSRWSACACATYTCMGCMKTRYVTSMG	500
LV DRF3	G..C....TC...G....AGCGA.....G.....T..C..AG.....T..A...G..AT.TAC.GGAC.....C...C..AT.ATA.GC.	495
VR2385 DRF3	T..A....AT..T....TCAAG.....A.....C..T.T.....G..G..CA.C...T..GC.CCA.CATG.....T..A..CG.GCT.CA.	498

FIG. 21B

Consensus	RCMTATTACCASCAYCARRTMGACGGGGCAATTGGTTTCAYYTRGAATGGSTGGCKCCMYTCTTTTCYTCYTGGYTGGTKYTMAYRTMTCWTGGTTTC	600
LV DRF3	G, A, . . . . . C, . C, . AA, A, . . . . . C, . TT, G, . . . . . C, . . . . . G, . AC, . . . . . T, . C, . . . . . GC, C, . . . . . CA, A, . . . . .	595
VR2385 DRF3	A, C, . . . . . G, . T, . GG, C, . . . . . T, . CC, A, . . . . . G, . . . . . T, . CT, . . . . . C, . T, . . . . . TT, A, . . . . . TG, C, . T, . . . . .	598
Consensus	TSAGGCGTTCGCCGTGYAAGCCMTGTTTCWSKWCGMRCTCTWCAGAYATYRAGACCAACACSACCGRGCKGCMGGYTTYRYKGTCTCYCARGACATCART	700
LV DRF3	, G, . . . . . T, . . . . . TCGA, . CA, . . . . . T, . TG, . . . . . G, . . . . . G, . T, . C, . . . . . T, . CATG, . . . . . T, . G, . . . . . A, . . . . .	695
VR2385 DRF3	, C, . . . . . C, . . . . . A, . . . . . AGTT, . AG, . . . . . T, . . . . . C, . CA, . . . . . C, . . . . . A, . G, . A, . C, . . . . . TGCT, . . . . . C, . A, . . . . . G, . . . . .	698
Consensus	TGYYTYMGRCMTCACGGSRWCTCRGCAGCKCAWGAGRMRAATTCCTTCGSAAGTCGYCYCARTIGYCGYGAMGSCGWYRGTACTCCCCAGTACATCACGA	800
LV DRF3	, . . TT, CC, A, C, . . . . . GGT, . . . . . A, . . . . . G, . . . . . AAA, . . . . . G, . . . . . T, . C, . A, . . . . . T, . A, . C, . . . . . TCG, . . . . .	795
VR2385 DRF3	, . . CC, TA, G, A, . . . . . CAA, . . . . . G, . . . . . T, . -T, . . . . . GCCG, . . . . . C, . . . . . -C, . T, . G, . C, . C, . G, . . . . . ATA, . . . . .	765
Consensus	TAA	803
LV DRF3	...	798
VR2385 DRF3	---	765

FIG. 21B.1



	Consensus	ATGGSTGGCGKCCMYTCTTTTCYTCYTCYTGCTGKYTMAAYRIMTCWTGGTTTCTSAGGCGTTCCGCTGYAAGCCMIGTTTCWSKWCGRCTCTWTCAGAYA	100
VR2385	DRF4	....G...T..CT.....C..T...T...TT..A...TG..C..T.....C.....C.....A.....AGTT...AG...T.....C..100	100
LV	DRF4	....C....G...AC.....T..C...C....GC..C...CA..A..A.....G.....T.....C.....TCGA..CA...A.....T..100	100

Consensus	TYRAGACCAACAC	SACCG	CGCGCKG	CGG	YTYRYK	GTCTCT	C	ARG	ACAT	CA	TTG	YYTYM	GC	MT	C	ACG	GS	W	CT	CG	CAG	CK	CA	W	AG	CM	RA	TT	CT	200		
VR2385	CA	.....	C	.....	A	G	A	C	..	TGCT	.....	C	A	.....	G	..	CC	TA	G	A	..	---	CAA	..	G	..	---	T	..	GCG	-----	189
LV	TG	.....	G	.....	G	T	C	T	..	CATG	.....	T	G	.....	A	..	TT	CC	A	C	.....	GGT	..	A	.....	G	A	..	AAA	.....	200	

Consensus	CGSAAAGTCGTCARTGCGYRMGGCSTMGKACWCCSWGATAYATCAKRTMACRCGYAAYGTACCAGGARWMWTAYTTIGYAYVMCKCKEAYCTK	300
VR2385 DRF4	. . C. . . . . -C. T. . G. . C. . CACG. . GA. A. . G. . A. . GT. . . . . T. . . . . TG. C. . A. . C. . T. . T. . . . . T. . . . . T. . . . . TTC. T. T. . T. . . . . T	288
LIV DRF 4	. . G. . . . . . . T. C. . A. . T. . TGAA. . CG. C. . T. . T. . CA. . . . . C. . . . . GA. A. . G. . T. . C. . G. . . . . C. . ATCA. . C. . . . . T. CAA. G. G. . C. . . . . G	300

	Consensus	CTSATGCTTTCTKCTGCCTTTTCTAYGCYTCWGARATGAGYGARAARGMITYAARGTSRTMTTGGSAATGTSTCWGGCRTCYGTGKKCWGYKTYGTGCA	400
VR2385	DRF4	..C.....T.T.....T.T.T..G....T..A..G..A..T..G..GG.A....C....G..A..A..C..GG.A.TG..C....	388
LV	DRF4	..G.....G.G.....C.C.A.A.....C.C.A..C..C..A..CA.C.....G.....C..T...G..T..T.T.CT..T....	400

Consensus	AYTTCACMRRTTAYGTSSMMCATGTC AAGGAATTACCCAACATACCCAGCAGYATCAYTTGGTARTTGAYCAYRTKGGYTGCTSCATTTCMTGACRCC	500
VR2385 DRF4	. C. .... CAG. . . C. CCAA. .... T. -, -CT. .... G. .... C. . TG. G. . . C. .... A. . . G. . .	476
IV DRF4	. T. .... AGA. . . T. GGCC. .... C. .... TC. .... A. . . T. CA. T. . . T. G. .... C. .... A. . .	491

Consensus	MMKMKRCMATGAGGTGGGGCWACWRYVWTWGCYGTGYTKTYRCCATTCTSTTGGCAATWTGA	561
VR2385 DRF4	CGAGA, C, . . . . . A, . TGTT, A, . C, . . C, T, . TA, . . . . . G, . . . . . T, . .	537
LV DRF4	ATCTG, A, . . . . . T, . AACCA, T, . T, . . T, G, . CG, . . . . . C, . . . . . A, . .	552

FIG. 21C

Consensus	M. WG. C., K., . . . . . L., . . . . . W., . . . . . L., . . . . . P. CL. SPSQ. G. WSF. S. WFAPR. SVRALPFTL. NYRRSYE., L., C., D. P., . . . . . KH	100
LV DRF2,	. Q., H. GV. SASCSWTPS. SSLLV. LI-----, PF., ---, Y., G., . . . . . D. Y., . . . . . F. E., . . . . . P., . . . . . GL. PN. RP. V. QFAV., .	90
VR2385 DRF2,	. K., L., --, -----AFLTK. AN-FL. MLSSSWCP. LI., YFW. F., A., . . . . . V. W., . . . . . A. D., . . . . . Y., . . . . . S., . . . . . AF. SQ. QV. I. TWGT., .	93
Consensus	PLGM. WH., VS. LIDEMVSRR. Y., ME., . GGAANKQVV. EATL., . . . . . S. LD. V. HFQHLLAA. EA., C., L. SRL. ML., L., . . . . . NV., . . . . . YN. TL., V., . . . . .	200
LV DRF2,	. . . . . F., MR., H., . . . . . I. QT., HS., . . . . . G., . . . . . TKL. G., I. T., . . . . . V., . . . . . DS. RF. S., . . . . . V., KN. AV--G., SLQ., T., . . . . . DR. ELI	188
VR2385 DRF2,	. . . . . L., HK., T., . . . . . M. RI., KA., . . . . . S., . . . . . SRI. S., V. A., . . . . . I., ET. KY. A., . . . . . P., HH. RMTGS., TIV., S., . . . . . NQ. FAV	193
Consensus	FPTPG. RPKL. DF. QWLI. VH. SIFSSVA. S. TLF. VLWLR. P. LR. VFGF. W., A., . . . . .	264
LV DRF2,	. . . . . T., . . . . . T., R., . . . . . S., A., . . . . . S. V., . . . . . I., . . . . . I. A., Y., . . . . . H. PT., ---THSS	249
VR2385 DRF2,	. . . . . S., . . . . . H., Q., . . . . . A., S., . . . . . A. C., . . . . . V., . . . . . V. M., T., . . . . . R. LG. IFLNSR-	257

FIG. 22A

Consensus	MA., C., FLC., Y., A., S., T., CFWFPL., GN, SFELT, NYT, C, PC, T, QAA., EPGR., WC, IGHDRC, E, DHDEL., PSG.,	100
LV DRF3,	., HQ, ARHF., GFIC, LVHS, LASN, SS, L., AH., T., I., I, M., S, S., RQRL., NM., K., E, R., LMSI., YDN	100
VR2385 DRF3,	., NS, TFLYI., CSFL, SFCC, VWAG, NA, Y., VR., F., V., V, P., L, R., AEAY., SL., R., G, D., GFVV., LSS	100
Consensus	., L., YAWLA, LSFSY, AQFHPE, FGIGNSV, VD., HQFICA, HDG, N, T., NISA., YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL	200
LV DRF3,	L-K, EGY., F., A., L., F., KR., E., H, S, VSTGH., LYAA., H., I., L., L., I.,	199
VR2385 DRF3,	EGH, TSA., S., T., I., Y., IK., V., Q, T, LPHHD., VLQT., Q., V., V., F., V.,	200
Consensus	RRSP, S, VS, R., Q., RPT, P., S., TS., L., R., F., K., S.,	266
LV DRF3,	., V, P., R, IY, IL., R, RLPVSW, FR., IVSD, TGSQQRK, K, PSES RPNV, P, VLPSTSR	265
VR2385 DRF3,	., A, H., V, VF, TS., P, QRQALL, SK., V--A, GIATRPL, R, A-----, -LSAARR-	255

## FIG. 22B

Consensus	M, A., LF, L, G., VS, AFACKPCFS., LSDI, TNTAAAGF, VLQDI, C, R., A, E., I., K., QCR, A, GTP, YIT, TANVTDE, YL., DL	100
LV DRF4,	., A, AT., F, A, AQHIM., E., TH., E., M., N, F, PHGVSA, Q, K, SFG, SS., E, V., Q., I., S., YNA.,	100
VR2385 DRF4,	., G, SL., L, V, FKCLL., Q., SS., K., A., S, L, HR--NS, S, A, R--, VP., T, I., V., V., N., HSS.,	96
Consensus	LMLS, CLFYASEMSEKGFKV, FGNVSG, V., CVNFT, YV, HV., TQ., V., RLLHF, TP., MRWAT., ACLF, ILLAI.,	184
LV DRF4,	., A., V, SA., D., A., TQH., QHHL, IDHI., L., SA., TI., A.,	183
VR2385 DRF4,	., S., V., I, AV., S., Q., KEF., RSLV, DH-V., M., ET., VL., T.,	179

## FIG. 22C

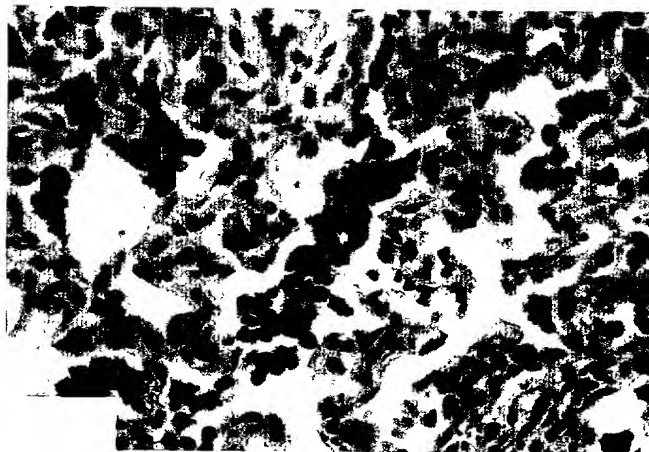


FIG.23

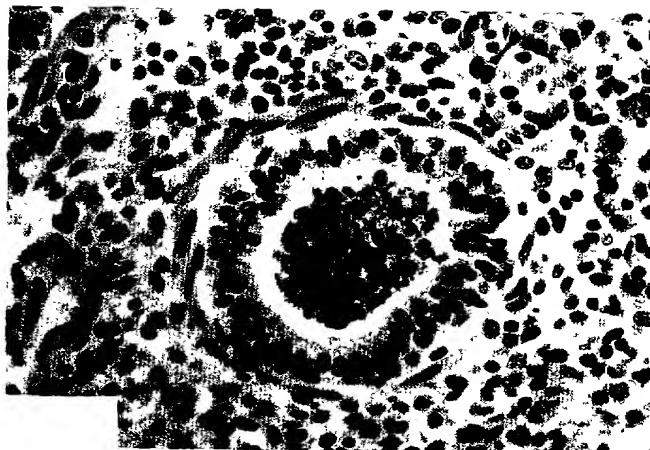


FIG.24

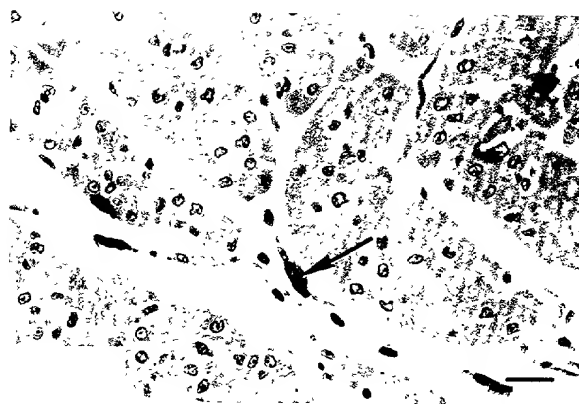


FIG.25

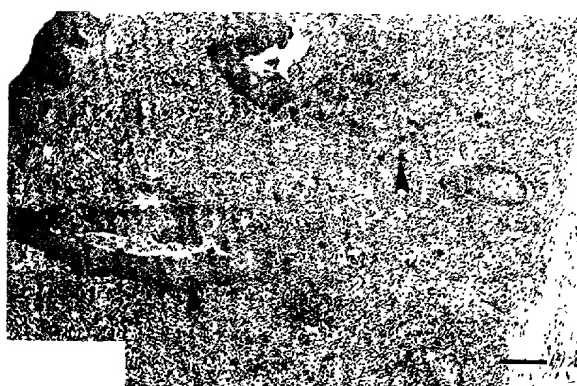


FIG.26

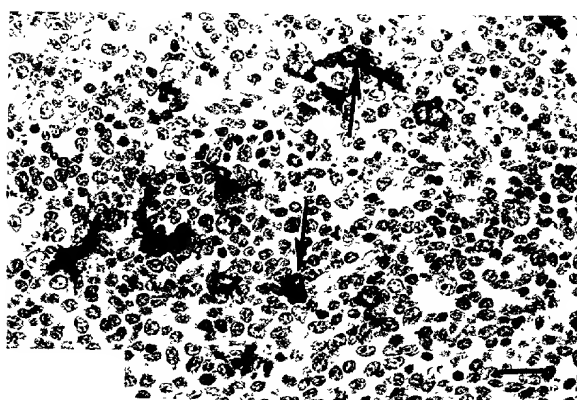


FIG.27



FIG. 28A



FIG. 28B



FIG. 28C

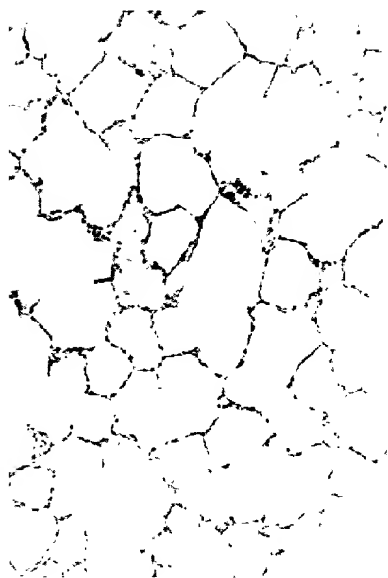


FIG. 29A



FIG. 29B



FIG. 29C



1894 3927

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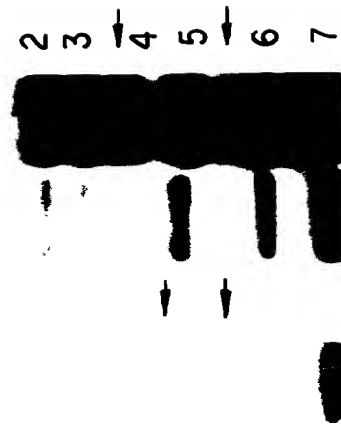


FIG.30A



FIG.30B